

FIG 1

ADAMTS-E nucleotide sequence [SEQ ID NO: 1]

CACGCGTCCGACGGCGCGGAGGCCCGGGCGCGGCGCAGGAGCCCGGTGAT
5 GCTGCGAAGGCTGTGAACAGGGGAGGCGGCACTGTGGGGGCTGCCGGCAGCCGGGG
CTGGGGAGAGACATGTGGACACGTGGCCTCTATGGCTCCCGCCTGCCAGATCCTCCGC
TGGGCCCTCGCCCTGGGGCTGGGCCTCATGTTGAGGTCACGCACGCCTTCCGGTCTC
AAGATGAGTTCTGTCCAGTCTGGAGAGCTATGAGATCGCCTTCCCCACCCGCGTGGAC
CACAACGGGGCACTGCTGGCCTTCTCGCCACCTCCTCCCCGGAGGCAGCGCCGCGGC
10 ACGGGGGCCACAGCCGAGTCCCGCCTCTTCTACAAAGTGGCCTCGCCCAGCACCCACT
TCCTGCTGAACCTGACCCGCAGCTCCCGTCTACTGGCAGGGCACGTCTCCGTGGAGTA
CTGGACACGGGAGGGCCTGGCCTGGCAGAGGGCGGCCCGGCCCACTGCCTCTACGC
TGGTCACCTGCAGGGCCAGGCCAGCACCTCCCATGTGGCCATCAGCACCTGTGGAGGC
CTGCACGGCCTGATCGTGGCAGACGAGGAAGAGTACCTGATTGAGCCCTGCACGGTG
15 GGCCCAAGGGTTCTCGGAGCCCGGAGGAAAGTGGACCACATGTGGTGTACAAGCGTTC
CTCTCTGCGTCACCCCCACCTGGACACAGCCTGTGGAGTGAGAGATGAGAAACCGTGG
AAAGGGCGGCCATGGTGGCTGCGGACCTTGAAGCCACCGCCTGCCAGGCCCTGGGG
AATGAAACAGAGCGTGGCCAGCCAGGCCTGAAGCGATCGGTCAGCCGAGAGCGCTACG
TGGAGACCCTGGTGGTGGCTGACAAGATGATGGTGGCCTATCACGGGCGCCGGGATGT
20 GGAGCAGTATGTCCTGGCCATCATGAACATTGTTGCCAACTTTTCCAGGACTCGAGTCT
GGGAAGCACCGTTAACATCCTCGTAACTCGCCTCATCCTGCTCACGGAGGACCAGCCCA
CTCTGGAGATCACCCACCATGCCGGGAAGTCCCTGGACAGCTTCTGTAAGTGGCAGAAA
TCCATCGTGAACCACAGCGGCCATGGCAATGCCATTCCAGAGAACGGTGTGGCTAACCA
TGACACAGCAGTGCTCATCACACGCTATGACATCTGCATCTACAAGAACAACCCCTGCG
25 GCACACTAGGCCTGGCCCCGGTGGGCGGAATGTGTGAGCGCGAGAGAAGCTGCAGCG
TCAATGAGGACATTGGCCTGGCCACAGCGTTCACCATTGCCACGAGATCGGGCACACA
TTCGGCATGAACCATGACGGCGTGGGAAACAGCTGTGGGGCCCGTGGTCAGGACCCAG
CCAAGCTCATGGCTGCCACATTACCATGAAGACCAACCCATTCTGTGTGGTCATCCTGC
AGCCGTGACTACATCACCAGCTTTCTAGACTCGGGCCTGGGGCTCTGCCTGAACAACCG
30 GCCCCCAGACAGGACTTTGTGTACCCGACAGTGGCACCGGGCCAAGCCTACGATGCA
GATGAGCAATGCCGCTTTCAGCATGGAGTCAAATCGCGTCAGTGTAATACGGGGAGGT
CTGCAGCGAGCTGTGGTGTCTGAGCAAGAGCAACCGGTGCATCACCAACAGCATCCCG
GCCGCCGAGGGCACGCTGTGCCAGACGCACACCATCGACAAGGGGTGGTGCTACAAAC
GGGTCTGTGTCCCCTTTGGGTGCGGCCAGAGGGTGTGGACGGAGCCTGGGGGCCGT
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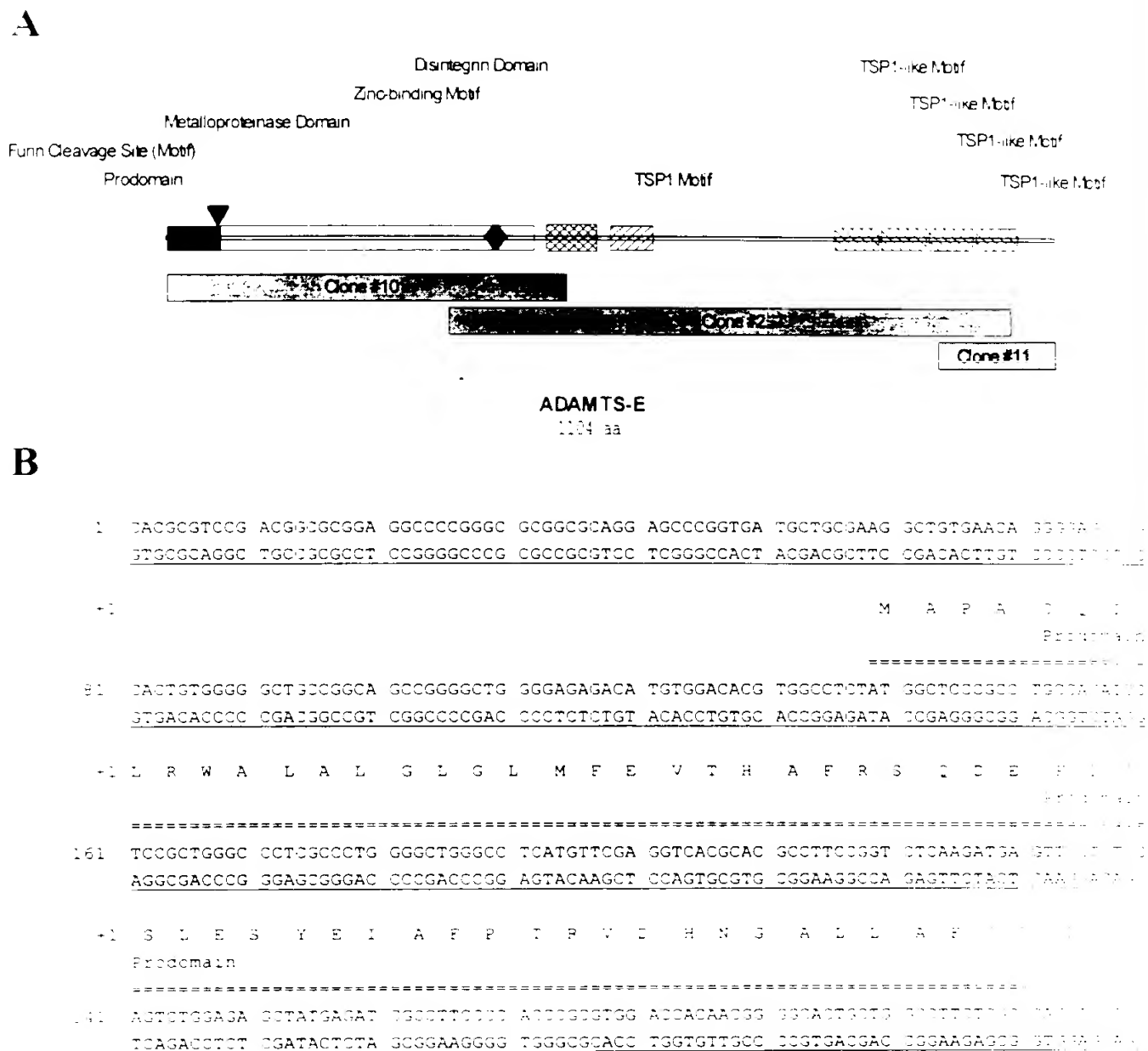
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TCTACACGGAGAGGGCGGCAGCCGTGGTGGACGGGACACCCTGCCGTCCAGACACGG
TGGACATTTGCGTCAGTGGCGAATGCAAGCACGTGGGCTGCGACCGAGTCCTGGGCTC
5 CGACCTGCGGGAGGACAAGTGCCGAGTGTGTGGCGGTGACGGCAGTGCCTGCGAGAC
CATCGAGGGCGTCTTCAGCCCAGCCTCACCTGGGGCCGGGTACGAGGATGTCGTCTGG
ATTCCCAAAGGCTCCGTCCACATCTTCATCCAGGATCTGAACCTCTCTCTCAGTCACTTG
GCCCTGAAGGGAGACCAGGAGTCCCTGCTGCTGGAGGGGCTGCCCGGGACCCCCCAG
CCCCACCGTCTGCCTCTAGCTGGGACCACCTTTCAACTGCGACAGGGGCCAGACCAGG
10 TCCAGAGCCTCGAAGCCCTGGGACCGATTAATGCATCTCTCATCGTCATGGTGCTGGCC
CGGACCGAGCTGCCTGCCCTCCGCTACCGCTTCAATGCCCCCATCGCCCGTGA CT CGC
TGCCCCCCTACTCCTGGCACTATGCGCCCTGGACCAAGTGCTCGGCCAGTGTGCAGG
CGGTAGCCAGGTGCAGGCGGTGGAGTGCCGCAACCAGCTGGACAGCTCCGCGGTGCG
CCCCCACTACTCCAGTGCCCCACAGCAAGCTGCCCAAAGGCAGCGCGCCTGCAACACG
15 GAGCCTTGCCCTCCAGACTGGGTTGTAGGGA ACTGGTCGCTCTGCAGCCGCAGCTGCG
ATGCAGGCGTGCGCAGCCGCTCGGTGCTGTGCCAGCGCCGCGTCTCTGCCGCGGAGG
AGAAGGCGCTGGACGACAGCGCATGCCCGCAGCCGCGCCACCTGTACTGGAGGCCT
GCCACGGCCCCACTTGCCCTCCGGAGTGGGCGGCCCTCGACTGGTCTGAGTGCACCC
CCAGCTGCGGGCCGGGCTCCGCCACCGCGTGGTCCTTTGCAAGAGCGCAGACCACC
20 GCGCCACGCTGCCCCCGGCGCACTGCTACCCGCCGCCAAGCCACCGGCCACCATGC
GCTGCAACTTGCGCCGCTGCCCCCGGCCCGCTGGGTGGCTGGCGAGTGGGGTGAGT
GCTCTGCACAGTGCGGCGTCGGGCAGCGGCAGCGCTCGGTGCGCTGCACCAGCCACA
CGGGCCAGGCGTCGCACGAGTGACGGAGGCCCTGCGGCCGCGGACTACCACGCAGC
AGTGTGAGGCCAAGTGCGACAGCCCAACCCCCGGGGACGGCCCTGAAGAGTGCAAGG
25 ATGTGAACAAGGTCGCCTACTGCCCCCTGGTGCTCAAATTTAGTTCTGCAGCCGAGCC
TACTTCCGCCAGATGTGCTGCAAAACCTGCCAGGGGCCACTAGGGGGCGCGCGGCACCC
GGAGCCACAGCTGGCGGGGTCTCCGCCGCCAGCCCTGCAGCGGGCCGGCCAGAGGG
GGCCCCGGGGGGGGCGGGA ACTGGGAGGGAAGGGTGAGACGGAGCCGGAAGTTATTT
ATTGGGAACCCCTGCAGGGCCCTGGCTGGGAGGATCCACCCCAACCTCTGCCCTGCCC
30 GCCCCAGGGGCACCCCGACATCCAGGCCACCCCTCATGGTGCTACAGACCCTGCCCT
GGGGCCACACACTCCTGCCAGGAAGCCCTACATCAATAAAGTTCTGTCTTGTGTAGAT
TTCTAAAAAAAAAAAAAAAA

FIG 2

ADAMTS-E amino acid sequence [SEQ ID NO: 2]

MAPACQILRWALALGLGLMFEVTHAFRSQDEFLSSLESYEIAFPTRVDHNGALLAFS
PPPPRRQRRGTGATAESRLFYKVASPTHFLLNLTRSSRLLAGHVSVEYWTREGLA
5 WQRAARPHCLYAGHLQGQASTSHVAISTCGGLHGLLIVADEEEYLIPLHGGPKGSR
SPEESGPHVVYKRSSLRHPHLDTACGVRDEKPPWKGRPWWLRTLKPPPARPLGNE
TERGQPGLKRSVSRERYVETLVVADKMMVAYHGRRDVEQYVLAIMNIVAKLFQDSS
LGSTVNILVTRLILLTQPTLEITHHAGKSLDSFCKWQKSIVNHS GHGNAIPENGVA
NHDTAVLITRYDICIYKNKPCGTLGLAPVGGMCERERSCSVNEDIGLATAFTIAHEIG
10 HTFGMNHGDBGVNSCGARGQDPAKLMAAHITMKTNPFWSSCSRDIYTSFLDSGLG
LCLNNRPPRQDFVYPTVAPGQAYDADEQCRFQHGKSRQCKYGEVCSELWCLSK
SNRCITNSIPAAEGTLCQHTIDKGWCYKRVCPFGSRPEGVDGAWGPWTPWGDC
SRTC GGGVSSSSRHCDSPRPTIGGKYCLGERRRHRSCNTDDCPPGSQDFREVQC
SEFDSIPFRCKFYKWKTYRGGGVKACSLTCLAEGFNFYTERAAAVDGTPCRPDV
15 DICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEGVFSPASPGAGYEDV
VWIPKGSVHIFIQDLNLSLSHLALKGDQESLLEGLPGTPQPHRLPLAGTTFQLRQGP
DQVQSLEALGPINASLIVMVLARTELPALRYRFNAPIARDSLPPYSWHYAPWTKCSA
QCAGGSQVQAVECRNQLDSSAVAPHYCSAHSKLPKRQRACNTEPCPPDWVVG
WSLCSRSCDAGVRSRVCQRRVSAAEEKALDDSA CPQPRPPVLEACHGPTCPPE
20 WAALDWSECTPSCGGLRHRVVLCKSADHRATLPPAHCSPA AKPPATMRCNLRR
PPARWWAGEWGECSAQCGVGQRQSVRCTSHTGQASHECTEALRPPTTTQQCE
AKCDSPTPGDGPEECKDVNKVAYCPLVLKFQFCSRAYFRQMCKCTCQGH

Figure 3. Domain structure of ADAMTS-E and translated nucleic acid sequence. A) Diagram of ADAMTS-E showing the following domains and signature motifs (with amino acid numbers in parentheses): prodomain (1-66), furin cleavage site (63-66), metalloproteinase domain (67-453), zinc-binding motif (392-420), disintegrin domain (469-531), TSP1 motif (548-601), and four TSP1-like motifs (829-884, 888-944, 948-1002, and 1007-1058). Overlapping clones covering the indicated sequence segments are depicted at the bottom of the diagram. **B)** ADAMTS-E nucleotide sequence with translated amino acid sequence above.



[illegible]

+1 G T G G G G G G G T T N I L A I F L I L L T E
Metalloproteinase Domain

101 GTAGAGCAT GTAGTGTGG AGGATGCTT AGAGATGTTT TAAATGCTT GATTTGTTT AATG
AAATGTTTGA GTTCAAGATG TTCTTGGGA GTATAGAGT ATTGATGGA GTATAGATG

+1 A I T H H A I F S L I F F I F W I Y I I
Metalloproteinase Domain

1061 GAGATGACG GAGGATGCGG GGAATGCTT GAGATGCTT TGAATGCTT AGAATGCTT
AGTGTAGTGG GTGTAGCGG GGTGTAGGGA GTGTGGAAG ACATGACGG GTGTAGGTA GTATGCTT

+1 G N A I P E N G V A N H D T A V L I T P Y D I I
Metalloproteinase Domain

1101 GCAATGCGAT TCCAGAGAAC GGTGTGGCTA AGCATGACAT GCAATGCTT ATCAGCGGT ATGATGCTT
GTGTAGGTA AGGTGCTTGG GCAAGCGAT TGGTACTGT GTGTAGGTA TAGTGTGGA TACTGTAGT

+1 N K P C G T L G L A P V G G M C E R E R S C S A A E
Metalloproteinase Domain

1201 AACAAACGCT GCGGCACACT AGGCTGCGG GCGTGGGGG GAATGTGTGA GCGGAGAGA AGCTGCGGT
GTGTGTTGGA GCGGTGTGA TCGGAGCGG GCGGAGCGG GTTACACACT GCGGTGCTT TCGAGTGTG

+1 I G L A T A F T I A H E I G H T F G M N H D S
Metalloproteinase Domain
Zinc-binding Motif

1291 GATTGGCCTG GGCACAGCGT TCACCATGCG GACGAGATC GGGCACACAT TCGGCATGAA GATGAGCGG
GTACCGGAC GCGTGTGCA AGTGGTAACG GGTGTGTAG GCGGTGTGA AGCGTACTT GGTACTGCG

+1 S C G A R G Q D P A K L M A A H I T M K T N P F
Zinc-binding Motif

1361 GCTGTGGGGC CCGTGGTCAG GACCCAGCCA AGCTCATGGC TGCCACATT ACCATGAAGA GCAACGATT
GACACCCCG GGCACAGTC CTGGGTGGT TCGAGTACCG ACGGGTGTA TGGTACTTCT GGTGGGTAA

+1 S C S R D Y I T S F L D S G L G L G L N N R P I
Metalloproteinase Domain

1441 TCGTGCAGCC GTGACTACAT GAGGATGCTT GTAGATGCG GCGTGGGGT GTGTGGAAG AATG
AGGAGCTCG GACTGATGTA GTGTGGAAG GTGTGGAAG GAGGATGCTT GTGTGGAAG

+1 F V Y P T V A P G Q A Y D A D E Q C R F Q H S
Disintegrin Motif

1501 GTTGTGTAC GGCAGAGTG GACCGGGCCA AGCTAGCAT GCAGATGAGC AATGCGGCTT TCGATGCGA
GAAACATG GCGTGTGACC GTGGGCGGT TCGATGCTA GGTGTACTG TTACGGCGAA AGTGTACTG

1001 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Disintegrin domain

1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020
1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040

1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060
Disintegrin domain

1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080
1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100

1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120
Disintegrin domain

1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140
1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160

1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180
TSPI Motif

1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200
1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220

1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240
TSPI Motif

1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260
1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280

1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300
1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320

1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340
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1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380
1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400

1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420
1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440

1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460
1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480

1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500

Fig. 4

Metalloproteinase Domain Alignment of ADAMTS-E v. ADAMTS Family

Percent Homology

34 AB014588	144	GLTAP---	LEETLAFAGKLLALELDAQVQVGLTQVIGGAF	ELDAPETLTLTNGEP	SALW
35 AF142099	144	IGGLISGG	FVYLVYGNFELLLEEDGVVGIAGEVAVGGGTA	ELWEP	TVAP
36 AF060152	144	GHGTR---	LRHAEQDLDELRLDDEFLAIGFTQNVGFS	GLLETLTANCHY	TVIGEP
37 AF140674	144	10PQAVS---	FLFFFLAYGHEHMLTINTVSHSHVEVWGLG	---	PWFHFLRCHYT
38 AF060153	144	---	GLAE---	---	GLDAROTTEVALSIC
39 AF060153	144	FTGNREEPGSHIF	YNTVTFEQLHRLRPNARLVAIGAEVGGG	---	TTTVEVETL
40 AF060153	144	GLATAES---	RQFFTVASFSTHLLNLTSSRLLEGLHVSVEVWTRG	---	LAWQVAPPHCY
Consensus	144		L L AFG F L L D A GET E G G	L C Y V L G P S AAL	
41 AB014588	149	LLGLQYKGA	LHLDFEG	---	THNSAGGIG
42 AF142099	149	LDGFFAVKHARV	TLKPRER	---	PWAEERGRVYG
43 AF060152	149	VRGAFYLLGSA	FLQPPAA	---	SERLATAAT
44 AF140674	149	PHAVIATED	EPKNT	---	TEDSRHSYENGH
45 AF060153	149	SGSFLLDG	FTQPOGAG	---	GSQAQHLQVWAG
46 AF060153	149	AGGLRMEET	EPPEP	---	LAQAQAEQGR
47 AF060153	149	HLIVADER	EPHCH	---	PKGSR
Consensus	149		E E Y I P L G G P HV K		
48 AB014588	154	LMNVKAPLQSPSP	PR-----	BAKRFAS	LSRF
49 AF142099	154	FAALASQLLDGALS	LAGGGQPTQWWR	RRKSI	RAEQ
50 AF060152	154	FWSPQDPALGV	CVCTGTG	---	SLKRF
51 AF140674	154	FWWINDTSTVSYSL	INNTHTHR	---	QKRS
52 AF060153	154	DFEESQEEAE	GAASEP	PLGA	---
53 AF060153	154	GSLLGLDLS	RALGVLEHANGS	---	RRARKHAAD
54 AF060153	154	WFHFWLRTL	KPPPARPLNENE	---	RGQGL
Consensus	154		P K ER VS R VETLLVAD	SMA FHG	L YLLTIM
55 AB014588	160	SVTALVT	NGSGEEGPOR	---	SAQVLRSE
56 AF142099	160	RAKVKVV	GDKRSL	---	SK
57 AF060152	160	SVKRLIV	HDEQKGP	---	TS
58 AF140674	160	RIEALIV	TEQPNL	---	INH
59 AF060153	160	EMVKV	LIVEDEKWP	---	SD
60 AF060153	160	SVL	TLILSYGFSMS	---	LEIGH
61 AF060153	160	SIUT	TLILTEQPTL	---	ETH
Consensus	160		EV NA TL NEQ WQ N P D FE		
62 AB014588	166	VLR	BSALVEDD	---	EQKFTAAHGLH
63 AF142099	166	LEP	BSGAMIEDD	---	PHAAFTVAH
64 AF060152	166	VLP	BSGAMIEDD	---	EQKFTAAHGLH
65 AF140674	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
66 AF060153	166	LEP	BSGAMIEDD	---	PHAAFTVAH
67 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
68 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
69 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
70 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
71 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
72 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
73 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
74 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
75 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
76 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
77 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
78 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
79 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
80 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
81 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
82 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
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91 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
92 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
93 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
94 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
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96 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
97 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
98 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
99 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH
100 AF060153	166	MEPR	BSGAMIEDD	---	EQKFTAAHGLH

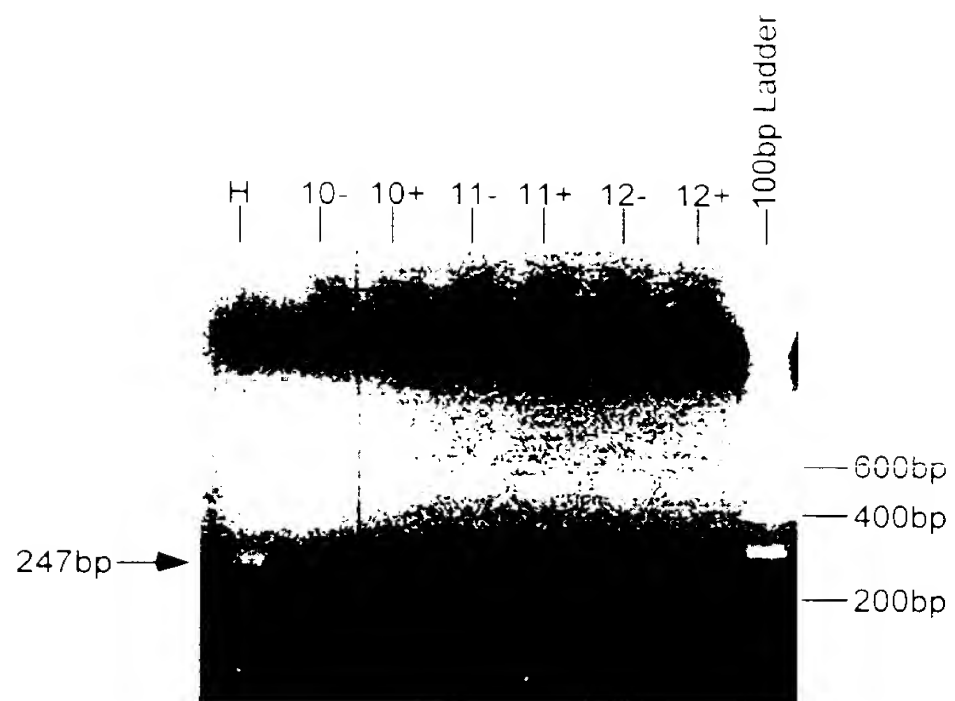


Figure 5. Expression of ADAMTS-E in cDNA from osteoarthritic cartilage.

Figure 6. Amino acid alignment of human ADAMTS-E with a GenScan prediction of ADAMTS-E from mouse genomic sequence.

		-----GASAPGAAALG--DAAPAVNRSGSTVGAAISFGWGETGSHVAIMAPACILPWAIAI -----GASAPGAAALG--DAAPAVNRSGSTVGAAISFGWGETGSHVAIMAPACILPWAIAI -----GASAPGAAALG--DAAPAVNRSGSTVGAAISFGWGETGSHVAIMAPACILPWAIAI
ADAMTS-E	101	LSLMEFYTHAFPSDEFLSLESYEIAFFTRVDHNGALLAFSPFRRQRRGTGATASSRLFYHVAIPETHFLINLH
ADAMTS-E	101	LSLMEFYTHAFPSDEFLSLESYEIAFFTRVDHNGALLAFSPFRRQRRGTGATASSRLFYHVAIPETHFLINLH
Consensus	101	LSLMEFYTHAFPSDEFLSLESYEIAFFTRVDHNGALLAFSPFRRQRRGTGATASSRLFYHVAIPETHFLINLH
ADAMTS-E	141	RLLAGHVSVEYWTREGLAWQRAARAHCLYAGHLQGQASTSHVAISTCGGLHGLIVADEEYLDHPLAGGHWG
ADAMTS-E	141	RLLAGHVSVEYWTREGLAWQRAARAHCLYAGHLQGQASTSHVAISTCGGLHGLIVADEEYLDHPLAGGHWG
Consensus	141	RLLAGHVSVEYWTREGLAWQRAARAHCLYAGHLQGQASTSHVAISTCGGLHGLIVADEEYLDHPLAGGHWG
ADAMTS-E	181	PHVYYRSSLRHPHLDTACGVDEFKPKWGRFWLRLTKPPPARPLGNETERGQPLRSVSREYVETLWADKMMWYH
ADAMTS-E	181	PHVYYRSSLRHPHLDTACGVDEFKPKWGRFWLRLTKPPPARPLGNETERGQPLRSVSREYVETLWADKMMWYH
Consensus	181	PHVYYRSSLRHPHLDTACGVDEFKPKWGRFWLRLTKPPPARPLGNETERGQPLRSVSREYVETLWADKMMWYH
ADAMTS-E	221	GRRDVECYVLAIMNI-----AKLFQDSSLGSTVNILVTRLILLTDDQPTLEITHHAGSLDSFCFWQKSIYH
ADAMTS-E	221	GRRDVECYVLAIMNI-----AKLFQDSSLGSTVNILVTRLILLTDDQPTLEITHHAGSLDSFCFWQKSIYH
Consensus	221	GRRDVECYVLAIMNI-----AKLFQDSSLGSTVNILVTRLILLTDDQPTLEITHHAGSLDSFCFWQKSIYH
ADAMTS-E	261	GHGNAIFENGVAHNDTAVLITPYDICIYKNKPCGTGLGLAPVGGMCERERSCSVNEDIGLATAFTIAHEIGHTFGMNHGV
ADAMTS-E	261	GHGNAIFENGVAHNDTAVLITPYDICIYKNKPCGTGLGLAPVGGMCERERSCSVNEDIGLATAFTIAHEIGHTFGMNHGV
Consensus	261	GHGNAIFENGVAHNDTAVLITPYDICIYKNKPCGTGLGLAPVGGMCERERSCSVNEDIGLATAFTIAHEIGHTFGMNHGV
ADAMTS-E	301	GNSCGAPGQDPAKLMAAHITMTNPFVWSSCSRDIYITSFLDSGLGLCLNNRPPRQDFVYPTVAPGQAYDAIEQCRFTHSV
ADAMTS-E	301	GNSCGAPGQDPAKLMAAHITMTNPFVWSSCSRDIYITSFLDSGLGLCLNNRPPRQDFVYPTVAPGQAYDAIEQCRFTHSV
Consensus	301	GNSCGAPGQDPAKLMAAHITMTNPFVWSSCSRDIYITSFLDSGLGLCLNNRPPRQDFVYPTVAPGQAYDAIEQCRFTHSV
ADAMTS-E	341	KSRQCFYGEVCSSELWCLSKSNFCITNSIFAAEGTLQTHITDKGWCYKPVCPFGSPPEGVDGAWGPWTPWGDCSRSCG
ADAMTS-E	341	KSRQCFYGEVCSSELWCLSKSNFCITNSIFAAEGTLQTHITDKGWCYKPVCPFGSPPEGVDGAWGPWTPWGDCSRSCG
Consensus	341	KSRQCFYGEVCSSELWCLSKSNFCITNSIFAAEGTLQTHITDKGWCYKPVCPFGSPPEGVDGAWGPWTPWGDCSRSCG
ADAMTS-E	381	GVSSSSPHCDSPRPTIGGKYCLGEPRRRHSCNTDCPPGSQDFREVQCSEFDSIPFRGKFFYWKTYRGGGVKACSLTCLA
ADAMTS-E	381	GVSSSSPHCDSPRPTIGGKYCLGEPRRRHSCNTDCPPGSQDFREVQCSEFDSIPFRGKFFYWKTYRGGGVKACSLTCLA
Consensus	381	GVSSSSPHCDSPRPTIGGKYCLGEPRRRHSCNTDCPPGSQDFREVQCSEFDSIPFRGKFFYWKTYRGGGVKACSLTCLA
ADAMTS-E	421	EGFNFYTERAAAVVDGTPCRPDTVDICVSGECKHVGC DRVLSGLREDKCRVCGGDSACETIEGVFSPALPGTYEDVV
ADAMTS-E	421	EGFNFYTERAAAVVDGTPCRPDTVDICVSGECKHVGC DRVLSGLREDKCRVCGGDSACETIEGVFSPALPGTYEDVV
Consensus	421	EGFNFYTERAAAVVDGTPCRPDTVDICVSGECKHVGC DRVLSGLREDKCRVCGGDSACETIEGVFSPALPGTYEDVV
ADAMTS-E	461	WIPKGSVHIFIQDLNLSLSHLALKGDQESLLEGLPGTPQPHRLPLAGTTFHRLRQGPDAQSLEALGPINASLIIMVLA
ADAMTS-E	461	WIPKGSVHIFIQDLNLSLSHLALKGDQESLLEGLPGTPQPHRLPLAGTTFHRLRQGPDAQSLEALGPINASLIIMVLA
Consensus	461	WIPKGSVHIFIQDLNLSLSHLALKGDQESLLEGLPGTPQPHRLPLAGTTFHRLRQGPDAQSLEALGPINASLIIMVLA
ADAMTS-E	501	DELPAFYRFNAPIARDLPPYSWHYAPWTKCSAQACAGGSQVQAVECRNQLDSSAVAPHYCSHSLPKRQRACTEPCE
ADAMTS-E	501	DELPAFYRFNAPIARDLPPYSWHYAPWTKCSAQACAGGSQVQAVECRNQLDSSAVAPHYCSHSLPKRQRACTEPCE
Consensus	501	DELPAFYRFNAPIARDLPPYSWHYAPWTKCSAQACAGGSQVQAVECRNQLDSSAVAPHYCSHSLPKRQRACTEPCE
ADAMTS-E	541	PDWVVGWNSLCSRSCDAGVRSFVVCQRPVSAAEKALDDSAQCPQPRPPVLEACHGPTCPPEWAALDWSECTPSGDFEL
ADAMTS-E	541	PDWVVGWNSLCSRSCDAGVRSFVVCQRPVSAAEKALDDSAQCPQPRPPVLEACHGPTCPPEWAALDWSECTPSGDFEL
Consensus	541	PDWVVGWNSLCSRSCDAGVRSFVVCQRPVSAAEKALDDSAQCPQPRPPVLEACHGPTCPPEWAALDWSECTPSGDFEL

HEWVLCKSADHRATLPPAHCPAAKPPATMRONLRROPPARWVAJEWGECDAJGNGGCHPQVPRCSTHTG...
HEWVLCKSADIRCTLEPCHOLPAANKPPATMRONLRROPPARWVTJEWGEC---GLGQCHPQVPRCSTHTG...
HEWVLCKSADIRCTLEPCHOLPAANKPPATMRONLRROPPARWVTJEWGEC---GLGQCHPQVPRCSTHTG...
R-PTTTCQCEAKCDSHPP-GDGPEECKDVNKVAYCPLVLKFGQCSRAYFROMCKTQGGH
R-PTTTCQCEAKCDSHPP-GDGPEECKDVNKVAYCPLVLKFGQCSRAYFROMCKTQGGH
R-PTTTCQCEAKCDSHPP-GDGPEECKDVNKVAYCPLVLKFGQCSRAYFROMCKTQGGH